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Best Local Similarity
Matches 831; Conserv
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Pfam; PF00023; Ank; 20.
PFINTS; PR01415; ANKYRIN.
SMART; SM00248; ANK; ARPEAT; 8.
PROSITE; PS50088; ANK REPEAT; 8.
PROSITE; PS50297; ANK REP REGION; 1.
SEQUENCE 1421 AA; 152990 MW; 60631
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Q9APN7;
01-JUN-2001
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"Novel Immunoreactive Glycoprotein Orthologs of Ehrlichia spp.";
Ann. N. Y. Acad. Sci. 0.0-0(2003).
EMBL; AF252298; AAK01145.2; -.
EMBL; O75332; 1QYM.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
MEDLINE=20579049; PubMed=11136790;
MCBride J.W., Corstvet R.E., Breitschwerdt E.B., Walker D.H.;
"Immunodiagnosis of Ehrlichia canis infection with recombinant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteria, Proteobacteria, Alphaproteobacteria, Rickettsiales,
Anaplasmataceae, Ehrlichia.
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                       WLTTSGPVRDIADRIVASKGDLSEDQVEEILDIIFMNESEIAEGISNPLHADVDNNPVKG
                                                                                              IGGVPQEAQYDAAARAGGPRKFLYGPYTFSNGQEINDFEFDTPWPDVRNAVLGNKEIKEE 180
                                                                                                                                               LERKSPTPEPKVEDDEDLPPTLPPRTFSGEGYDDVGVSMPTVSRGIYQPPIVQDSNLYSS
                                                                                                                                                                       LERKSPTPEPKVEDDEDLPPTLPPRTFSGEGYDDVGVSMPTVSRGIYQPPIVQDSNLYSS 120
                                                                                                                                                                                                                          WLTTSGPVRDIADRIVASKGDLSEDQVBEILDIIPMNESEIAEGISNPLHADVDNNPVKG
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                                                                                                                                                                                                                                                PSGDIQDQSQQDQQEQDQQQQAVGGAVGNSPIERERVAAPESEDLYTVIIPKGKRTAAPI 60
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(TrEMBLrel. 26, Last sequence update)
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                                                                                                                                                                                                                                                                                                 100.0%; Score 4310; DB 2; Length 1421; 100.0%; Pred. No. 1.1e-228; cive 0; Mismatches 0; Indels 0;
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ALIGNMENTS

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